REMARKS

1. Preliminary Remarks

a. Status of Claims

Claims 69-72, 89-96 are pending and under active consideration. Claims 69-72 are allowed. Claims 89 and 96 are amended. Claims 90, 91, 94, and 95 are canceled. Applicant respectfully requests entry of the amendments and remarks made herein into the file history of this application. Upon entry of the amendments, claims 69-72, 89, 92, 93, and 96 will be pending and under active consideration.

b. Amendment to the Claims

In order to expedite prosecution and without prejudice to seeking claims of similar scope in a continuing application, Applicant has canceled claims 90, 91, 94, and 95 without prejudice. Claim 89 has been amended in part (c), which is now directed to an isolated nucleic consisting of X nucleotides wherein the sequence of the nucleic acid comprises a sequence at least 80% identical to Y consecutive nucleotides of SEQ ID NO: 2 or 9, or an RNA encoded by Y consecutive nucleotides of SEQ ID NO: 2 or 9, wherein X= 19 to 140, Y≥19, and X≥Y. Support for amended claim 89 can be found throughout the specification, for example, paragraph 0049.

Claim 96 have been amended and is now directed to a vector comprising a heterologous sequence, wherein the heterologous sequence consists of the sequence of the nucleic acid of claims 69-72, 89, 92, 93, and 96. Support for amended claim 96 can be found throughout the specification, for example, paragraph 0039. One of ordinary skill in the art would recognize that features other than the heterologous sequence would be necessary for a functional vector.

2. Patentability Remarks

On pages 2-4 of the Office Action, the Examiner rejects claims 89-91 and 96 under 35 U.S.C. §112, first paragraph, for failing to comply with the written description requirement. Specifically, the Examiner asserts that the limitations "a sequence 68.2% identical to (a) or (b)," "a sequence at least 81.9% identical to (a) or (b)," and "a sequence at least 91.0% identical to (a) or (b)" lack support in the disclosure. Applicant respectfully traverses.

As acknowledged by the Examiner on page 4 of the Office Action, the specification describes that miRNAs can bind to target genes with less than 100% complementary, but asserts that the specification does not appear to provide a description sufficient to support a genus of molecules now encompassed by the claims. Applicant disagrees with regard to sufficient description. As discussed in our response filed June 11, 2007, the specification provides numerous examples of the claimed miRNAs as set forth in SEQ ID NOS: 2 and 9 binding target genes with less than 100% complementarity. For example, Table 7, lines 188035-188829 of the specification shows examples of the claimed miRNAs sequences as set forth in

SEQ ID NOS: 2 and 9 binding various target gene sequences with 68.2%, 81.9%, and 91.0% complementarity (See Appendix A).

The Examiner however states on page 3 of the Office Action that a text search of "68.2%, "81.9%", and "91.0%" was unsuccessful. Applicant submits that the alignments shown in Table 7 provide the inherent written descriptive support of these percent variants by calculating the percentage of the number of bases that align between the miRNA sequence and the target gene sequence. One of skill in the art can reasonably conclude that the inventor had possession of the claimed invention by the alignments described in Table 7.

Nevertheless, in order to expedite prosecution, claim 89 has been amended as described above because the specification does clearly provide textual support at paragraph 0049 for at least 80% variants of the claimed miRNA sequences as set forth in SEQ ID NOS: 2 and 9 that bind and repress expression of mRNA transcripts of particular target genes. As discussed above, claims 90 and 91 have been canceled without prejudice and claim 96 draws its dependency in part from claim 89. In view of the foregoing amendment and remarks, Applicant respectfully request that the rejection of claims 89-91 and 96 under 35 U.S.C. §112, first paragraph for allegedly lacking proper written description support has been overcome and should be withdrawn.

3. Conclusion

Applicant respectfully submits that the instant application is in good and proper order for allowance and early notification of to this effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the instant application, the Examiner is encouraged to call the undersigned at the number listed below.

Respectfully submitted,

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Dated: March 12, 2009

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APPENDIX A

Table 7, lines 188035-188829 disclose that the miRNA GAM3298 (SEQ ID NO: 2) is capable of binding to sites within 326 target gene mRNAs. Table 7 further discloses that 15 out of 22 nucleotides (68.2%) of GAM3298 are sufficient for binding target mRNAs. For example, 68.2% of the residues of SEQ ID NO: 2 are capable of targeting mRNAs of the genes HIP1 and ADCY1, as follows:

GAM NAME	GAM RNA SEQUENCE	TARGET REF-ID	TARGET	UTR	TARGET BS-SEQ (UPPER:GAM;LOWER:TARGET)	BINDING-SITE DRAW	GAM POS
GAM3298	AAAGTGCTCAT AGTGCAGGTAG	HIP1	NM_005338.3	3	ACGCCTGTAATCC CAGCACTTT	CATAG AG AAAGTGCT TGCAGGT TTTCACGA ATGTCCG CCCTA CA	A
GAM3298	AAAGTGCTCAT AGTGCAGGTAG	ADCY1	NM_021116.1	3	TGTTTGCACTATA CTTT	GCTC GG AAAGT ATAGTGCA TA TTTCA TATCACGT GT ---- TT	A

Table 7 also discloses that the mRNA GAM2608 (SEQ ID NO: 9) is capable of binding to sites within 117 target gene mRNAs. Table 7 further discloses that 15 out of 22 nucleotides (68.2%) of GAM2608 are sufficient for binding target gene mRNAs. For example, 68.2% of the residues of SEQ ID NO: 9 are capable of targeting mRNAs of the genes CALCB and EGR4, as follows:

GAM2608	TAAGGTGCATC TAGTGCAGTTA	CALCB	NM_000728.2	3	TAATTGCCCCTGC ACCTTT	T TCTAGT AAGGTGCA GCAGTTA TTCCACGT CGTTAAT T CCC---	A
GAM2608	TAAGGTGCATC TAGTGCAGTTA	EGR4	NM_001965.1	3	TAACTGCACACGC CCCACGCCTTC	T CATCTA-- AAGGTG GTGCAGTTA TTCCGC CACGTCAAT C ACCCCGCA	A

Table 7 discloses that 18 out of 22 nucleotides (81.9%) of the miRNA GAM3298 (SEQ ID NO: 2) are sufficient for binding target gene mRNAs. For example, 81.9% of the residues of SEQ ID NO: 2 are capable of targeting mRNAs of the genes ABCC3 and ADSL, as follows:

GAM3298	AAAGTGCTCAT AGTGCAGGTAG	ABCC3	NM_020037.1	3	TACCTGCACTGTC CTGACCATCGCAC	AAA ----- --- GTGC TCA TAGTGCAGGTA CACG AGT GTCACGTCCAT --- CTACC CCT	A
GAM3298	AAAGTGCTCAT AGTGCAGGTAG	ADSL	NM_000026.1	3	TTACCTTAAATTA GTACAGCACTTT	CA-- GC- AAAGTGCT TAGT AGGTAG TTTCACGA ATTA TCCATT CATG AAT	A

Table 7 also discloses that 18 out of 22 nucleotides (81.9%) of the miRNA GAM2608 (SEQ ID NO: 9) are sufficient for binding target gene mRNAs. For example, 81.9% of the residues of SEQ ID NO: 9 are capable of targeting mRNAs of the genes ABCC3 and CASP3, as follows:

```
GAM2608   TAAGGTGCATC ABCC3   NM_020038.1  3  TAGCAAACACTGG         AT      CA-             A
          TAGTGCAGTTA                         GGGCACCTTA    TAAGGTGC  CTAGTG   GTTA
                                                            ATTCCACG  GGTCAC   CGAT
                                                                    GG      AAA

GAM2608   TAAGGTGCATC CASP3   NM_032991.1  3  TAACTGCATTTTA TA     CA    --                A
          TAGTGCAGTTA                         GACCATTTAT      AGGTG  TCTA  GTGCAGTTA
                                                              TTTAC  AGAT  TACGTCAAT
                                                            TA     C-    TT
```

Table 7 discloses that 20 out of 22 nucleotides (91.0%) of the miRNA GAM3298 (SEQ ID NO: 2) are sufficient for binding target gene mRNAs. For example, 91.0% of the residues of SEQ ID NO: 2 are capable of targeting mRNAs of the genes ASTN and MECP2, as follows:

```
GAM3298   AAAGTGCTCAT ASTN    XM_045113.2  3  ATGCCAGGCGCTG         --   -     A-    G      A
          AGTGCAGGTAG                         ATGTAAGCACTTT AAAGTGCT  CAT AGTGC  GGTA
                                                            TTTCACGA  GTA TCGCG  CCGT
                                                                    AT   G     GA    A

GAM3298   AAAGTGCTCAT MECP2   NM_004992.2  3  TTATTTGCACTAT A   T     -                     A
          AGTGCAGGTAG                         TGAGTCTTC      AAG GCTCA TAGTGCAGGTAG
                                                             TTC TGAGT ATCACGTTTATT
                                                            C   -     T
```

Table 7 also discloses that 20 out of 22 nucleotides (91.0%) of the miRNA GAM2608 (SEQ ID NO: 9) are sufficient for binding target gene mRNAs. For example, 91.0% of the residues of SEQ ID NO: 9 are capable of targeting mRNAs of the genes MAP4K5 and MMP26, as follows:

```
GAM2608   TAAGGTGCATC MAP4K5  NM_006575.2  3  AAACTGCACTATG        C   -          A         A
          TAGTGCAGTTA                         ATTTGCTTTA    TAAGGTG ATC TAGTGCAGTT
                                                            ATTTCGT TAG ATCACGTCAA
                                                                   T   T          A

GAM2608   TAAGGTGCATC MMP26   NM_021801.2  3  AACTGAAAGCACT      -   A        ----          A
          TAGTGCAGTTA                         AGAGCAGCCTTG  TAAGG TGC TCTAGTGC    AGTT
                                                            GTTCC ACG AGATCACG    TCAA
                                                                 G   -        AAAG
```